

SEQUENCE LISTING



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#6/a  
TECH CENTER 1600/2900

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<110> Hinuma, Shujii  
<110> Kawamata, Yuji  
<110> Fujii, Ryo  
<110> Matsumoto, Hirokazu  
<120> Prolactin Secretion Modulator  
<130> 2472USOP  
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<150> PCT/JP98/02765  
<151> 1998-06-22  
<150> JP 9-165437  
<151> 1997-06-23  
<160> 99  
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<210> 1  
<211> 98  
<212> PRT  
<213> Bovine  
<400> 1

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu  
1 5 10 15  
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile  
20 25 30  
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Pro Gly Asp Gly Pro  
50 55 60  
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
65 70 75 80  
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val  
85 90 95  
Gln Glu

<210> 2  
<211> 294  
<212> DNA

<213> Bovine

<400> 2

ATGAAGGCGG TGGGGGCCTG GCTCCTCTGC CTGCTGCTGC TGGGCCTGGC CCTGCAGGGG 60  
GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA CCCCCGACAT CAACCCTGCC 120  
TGGTACGCRG GCCGTGGGAT CCGGCCCGTG GGCCGCTTCG GCCGGCGAAG AGCTGCCCYG 180  
GGGGACGGAC CCAGGCCTGG CCCCCGGCGT GTGCCGGCCT GCTTCCGCCT GGAAGGCGGY 240  
GCTGAGCCCT CCCGAGCCCT CCGGGGGCGG CTGACGGCCC AGCTGGTCCA GGAA 294

<210> 3

<211> 29

<212> PRT

<213> Bovine

<400> 3

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly  
20 25

<210> 4

<211> 19

<212> PRT

<213> Bovine

<400> 4

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg  
19

<210> 5

<211> 31

<212> PRT

<213> Bovine

<400> 5

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
20 25 30

<210> 6

<211> 32

<212> PRT

<213> Bovine

<400> 6

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30

<210> 7

<211> 33

<212> PRT

<213> Bovine

<400> 7

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30  
Arg  
33

<210> 8

<211> 20

<212> PRT

<213> Bovine

<400> 8

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe  
20

<210> 9

<211> 21

<212> PRT

<213> Bovine

<400> 9

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly  
20

<210> 10

<211> 22

<212> PRT

<213> Bovine

<400> 10

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly Arg  
20

<210> 11

<211> 87

<212> DNA

<213> Bovine

<400> 11

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60  
GCRGGCCGTG GGATCCGGCC CGTGGGC 87

<210> 12

<211> 57

<212> DNA

<213> Bovine

<400> 12

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGC 57

<210> 13

<211> 93

<212> DNA

<213> Bovine

<400> 13

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60  
GCRGGCCGTG GGATCCGGCC CGTGGGCCG TTC 93

<210> 14

<211> 96

<212> DNA

<213> Bovine

<400> 14

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCGG ACATCAACCC TGCCTGGTAC 60  
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGC 96

<210> 15

<211> 99

<212> DNA

<213> Bovine

<400> 15

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCGG ACATCAACCC TGCCTGGTAC 60  
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGCCG 99

<210> 16

<211> 60

<212> DNA

<213> Bovine

<400> 16

ACCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC 60

<210> 17

<211> 63

<212> DNA

<213> Bovine

<400> 17

ACCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC 60  
GGC 63

<210> 18

<211> 66

<212> DNA

<213> Bovine

<400> 18

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GGCCGG 66

<210> 19  
<211> 91  
<212> PRT  
<213> Human  
<400> 19

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn  
1 5 10 15  
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala  
20 25 30  
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val  
35 40 45  
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr  
50 55 60  
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr  
65 70 75 80  
Val Val Leu Val His Pro Leu Arg Arg Arg Ile  
85 90

<210> 20  
<211> 59  
<212> PRT  
<213> Human  
<400> 20

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu  
1 5 10 15  
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly  
20 25 30  
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg  
35 40 45  
Thr Phe Cys Leu Leu Val Val Val Val Val Val  
50 55

<210> 21  
<211> 370  
<212> PRT  
<213> Human  
<400> 21

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser  
1 5 10 15  
Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala  
20 25 30  
Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr  
35 40 45  
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val  
50 55 60  
Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu  
65 70 75 80  
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn



130 135 140  
Tyr Ala Trp Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val  
145 150 155 160  
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val  
165 170 175  
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
180 185 190  
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val  
195 200 205

<210> 23

<211> 126

<212> PRT

<213> Murine

<400> 23

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser  
1 5 10 15  
Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu  
20 25 30  
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val  
35 40 45  
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile  
50 55 60  
Tyr Ala Trp Gly Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala  
65 70 75 80  
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val  
85 90 95  
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
100 105 110  
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val  
115 120 125

<210> 24

<211> 273

<212> DNA

<213> Human

<400> 24

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACCTT CCTCATCGGC 60  
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCTGCG TGCCGCTCAC GCTGGCCTAT 120  
GCCTTCAGC CACGCGGCTG GGTGTTTCGGC GGCGGCTGT GCCACCTGGT CTTCTTCCTG 180  
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACCTCACCA CCATCGCAGT GGACCGGTAC 240  
GTCGTGCTGG TGCACCCGCT CAGGCGGCGC ATC 273

<210> 25

<211> 177

<212> DNA

<213> Human



<400> 25

GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGC 60  
GTGTCACTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120  
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

<210> 26

<211> 1110

<212> DNA

<213> Human

<400> 26

ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTTCTGG GCTGCCGCCG 60  
GCGCTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CCGGCAACGC GTCGGTGGCT 120  
GGCGCGGACG CTCAGCCCGT CAGGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180  
GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTTCGTG GGCTGGTGGG CAACTGCCTG 240  
CTGCTGCTGG TGATCGCGCG GGTCCGCCGG CTGCACAACG TGACCAACTT CCTCATCGGC 300  
AACCTGGCCT TGTCGACGCT GCTCATGTGC ACCGCCGCGG TGCCGCTCAC GCTGGCCTAT 360  
GCCTTCGAGC CAGCGGGCTG GGTGTTCGGC GGCGGCCGTG GCCACCTGGT CTTCCTCCTG 420  
CAGCCGGTCA CCGTCTATGT GTCCGTGCTC ACGCTACCA CCATCGGAGT GGACCGCTAC 480  
GTCGTGCTGG TGGACCCGCT GAGGCGGGCC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540  
CTGGCCATCT GGGCGCTGTC CGCGCTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 600  
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 660  
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720  
ATCCTCCTGT CTTACGTCCG GGTGTCACTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780  
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGACCTT CTGCTTGCTG 840  
GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGGTGCCCG TGCACGTCTT CAACCTGCTG 900  
CGGGACCTCG ACCCCAGGC CATCGACCTT TACGCTTTG GGCTGGTGCA GCTGCTCTGC 960  
CACTGGCTCG CCATGAGTTC GGCTGCTAC AACCCTTCA TCTACGCTG GCTGCAAGAC 1020  
AGCTTCGGCG AGGAGCTGCG CAAACTGTG GTGCTTGGC CCCGCAAGAT AGCCCCCAT 1080  
GGCCACAATA TGACCGTCAG CGTGGTCATC 1110

<210> 27

<211> 618

<212> DNA

<213> Murine

<400> 27

CTGGTGCTGG TGATGGCGCG GGTGCGCCGC CTGTACAACG TGACGAATTT CCTCATCGGC 60  
AACCTGGCCT TGTCGACGCT GCTCATGTGC ACGGCCTGCG TGCCGCTCAC GCTGGCCTAT 120  
GCCTTCGAGC CAGCGGGCTG GGTGTTCGGC GGCGCCCTGT GCCACCTGGT CTTCCTCCTG 180  
CAGGCGGTCA CCGTCTATGT GTCCGTGTTT ACGCTACCA CCATCGCAGT GGACCGCTAC 240  
GTCGTGCTGG TGCACCCGCT GAGGCGGGCC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300  
CTGGCCATCT GGGTGTGCTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 360  
GTGGAGCTCA AGCCGGACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420  
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480  
ATCCTCCTGT CTTAGGCCCG GCTGTCACTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 540  
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGGACCTT CTGCTTGCTG 600  
GTGCTGGTCG TGGTGGTG 618

<210> 28

<211> 378

<212> DNA

<213> Murine

<400> 28

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG 60  
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT 120  
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180  
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240  
ATCCTCCTGT CTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300  
GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360  
GTGGTGGTGG TGGTAGTG 378

<210> 29

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 29

CGTGGSCMFS STGGGCAACN YCCTG 25

<210> 30

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 30

GTNGWRRGGC ANCCAGCAGA KGGCAAA 27

<210> 31

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 31

CTGTGYGYS TYGCNNTKGA YMGSTAC 27

<210> 32

<211> 29

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 32

AKGWAGWAGG GCAGCCAGCA GANSRYGAA 29

<210> 33

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 33

CTGACTTATT TTCTGGGCTG CCGC 24

<210> 34

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 34

AACACCGACA CATAGACGGT GACC 24

<210> 35

<211> 20

<212> DNA

<213> Unknown

<220>

Onb  
B1  
C11

<223> Unsure

<400> 35

GCICAYCARC AYTGYATGGA 20

<210> 36

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 36

CCIACGGGIC KDATGCCICK GCCIGC 26

<210> 37

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 37

ACGGGCCCKDA TGCCICKGCC IGCRTA 26

<210> 38

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 38

CCGGCGTACC AGGCAGGGTT 20

<210> 39

<211> 28

<212> DNA  
<213> Unknown  
<220>  
<223> Unsure  
<400> 39  
AGGCAGGGTT GATGTCGGGG GTGCGGAT 28

<210> 40  
<211> 27  
<212> DNA  
<213> Unknown  
<220>  
<223> Unsure  
<400> 40  
CTGCCAGCAG AGCCCACCAG CACTCCA 27

<210> 41  
<211> 27  
<212> DNA  
<213> Unknown  
<220>  
<223> Unsure  
<400> 41  
GTGGGGGCCT GGCTCCTCTG CCTGCTG 27

<210> 42  
<211> 32  
<212> DNA  
<213> Unknown  
<220>  
<223> Unsure  
<400> 42  
GTGTCGACGA ATGAAGGCGG TGGGGGCCTG GC 32

<210> 43  
 <211> 24  
 <212> DNA  
 <213> Unknown  
 <220>  
 <223> Unsure  
 <400> 43

AGGCTCCCGC TGTTATTCCT GGAC 24

<210> 44  
 <211> 98  
 <212> PRT  
 <213> Bovine  
 <400> 44

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu  
 1 5 10 15  
 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile  
 20 25 30  
 Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
 35 40 45  
 Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Leu Gly Asp Gly Pro  
 50 55 60  
 Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
 65 70 75 80  
 Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val  
 85 90 95  
 Gln Glu

<210> 45  
 <211> 83  
 <212> PRT  
 <213> Rat  
 <400> 45

Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Leu Ser Leu Val  
 1 5 10 15  
 Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg  
 20 25 30  
 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
 35 40 45  
 Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly  
 50 55 60  
 Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser  
 65 70 75 80  
 Gln Arg Gly

<210> 46  
<211> 249  
<212> DNA  
<213> Rat  
<400> 46

ATGGCCCTGA AGAAGTGGCT TCTGTGCTTG CTGCTGCTAA GCTTGGTCCT CCCAGGGGCT 60  
TCCAGCCGAG CCCAQCAGCA CTCCATGGAG ACAAGAACCC CTGATATCAA TCCTGCCTGG 120  
TACACGGGCC GCGGGATCAG GCCTGTGGGC CGCTTCGGCA GGAGAAGGGC AACCCCGAGG 180  
GATGTCACTG GACTTGCCCA ACTCAGCTGC CTCCCACTGG ATGGACGCAC CAAGTTCTCT 240  
CAGCGTGGA 249

<210> 47  
<211> 31  
<212> PRT  
<213> Rat  
<400> 47

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
20 25 30

<210> 48  
<211> 32  
<212> PRT  
<213> Rat  
<400> 48

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30

<210> 49  
<211> 33  
<212> PRT  
<213> Rat  
<400> 49

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

Arg 20 25 30

<210> 50

<211> 20

<212> PRT

<213> Rat

<400> 50

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe  
20

<210> 51

<211> 21

<212> PRT

<213> Rat

<400> 51

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly  
20

<210> 52

<211> 22

<212> PRT

<213> Rat

<400> 52

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly Arg  
20

<210> 53

<211> 93

<212> DNA

<213> Rat

<400> 53

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCTG ATATCAATCC TGCCTGGTAC 60



ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTC

93

<210> 54

<211> 96

<212> DNA

<213> Rat

<400> 54

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAAGCCCTG ATATCAATCC TGCCTGGTAC 60  
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGC 96

<210> 55

<211> 99

<212> DNA

<213> Rat

<400> 55

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAAGCCCTG ATATCAATCC TGCCTGGTAC 60  
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGCAGG 99

<210> 56

<211> 60

<212> DNA

<213> Rat

<400> 56

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

<210> 57

<211> 63

<212> DNA

<213> Rat

<400> 57

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGC 63

<210> 58

<211> 66

<212> DNA

<213> Rat

<400> 58

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGCAGG 66

<210> 59

<211> 87

<212> PRT

<213> Human

<400> 59

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu  
1 5 10 15  
Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile  
20 25 30  
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro  
50 55 60  
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly  
65 70 75 80  
Ala Met Ser Ser Gln Asp Gly  
85

<210> 60

<211> 261

<212> DNA

<213> Human

<400> 60

ATGAAGGTGC TGAGGGCCTG GCTCCTGTGC CTGCTGATGC TGGGCCTGGC CCTGCGGGGA 60  
GCTGCAAGTC GTACCCATCG GCACTCCATG GAGATCCGCA CCCCTGACAT CAATCCTGCC 120  
TGGTACGCCA GTCGCGGGAT CAGGCCTGTG GGCCGCTTCG GTCGGAGGAG GGCAACCCTG 180  
GGGGACGTCC CCAAGCCTGG CCTGCGACCC CGGCTGACCT GCTTCCCCTT GGAAGGCGGT 240  
GCTATGTCGT CCCAGGATGG C 261

<210> 61

<211> 31

<212> PRT

<213> Human

<400> 61

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe

20

25

30

&lt;210&gt; 62

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 62

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

&lt;210&gt; 63

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 63

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

Arg

&lt;210&gt; 64

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 64

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe												
			20												

&lt;210&gt; 65

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 65

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1 5  
Val Gly Arg Phe Gly  
20

10

15

<210> 66

<211> 22

<212> PRT

<213> Human

<400> 66

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly Arg  
20

<210> 67

<211> 93

<212> DNA

<213> Human

<400> 67

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60  
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTC 93

<210> 68

<211> 96

<212> DNA

<213> Human

<400> 68

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60  
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGT 96

<210> 69

<211> 99

<212> DNA

<213> Human

<400> 69

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60  
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGTCCG 99

<210> 70

<211> 60

<212> DNA

<213> Human

<400> 70

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

<210> 71

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<400> 71

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GGT 63

<210> 72

<211> 66

<212> DNA

<213> Human

<400> 72

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGTCGG 66

<210> 73

<211> 21

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 10th position is Ala or Thr.  
Xaa of the 11th position is Gly or Ser.  
Xaa of the 21st position is H, Gly or GlyArg.

<400> 73

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Xaa  
20

<210> 74

<211> 11

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 3rd position is Ala or Thr.  
Xaa of the 5th position is Gln or Arg.  
Xaa of the 10th position is Ile or Thr.

<400> 74

Ser Arg Xaa His Xaa His Ser Met Glu Xaa Arg  
1 5 10

<210> 75

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

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CARCAYTCCA TGGAGACAAG AACCCC 26

<210> 76

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

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TACCAGGCAG GATTGATACA GGGG 24

<210> 77

<211> 25

<212> DNA

<213> Unknown

<220>

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GGCATCATCC AGGAAGACGG AGCAT 25

<210> 78

<211> 25

<212> DNA

<213> Unknown

<220>

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<400> 78

AGCAGAGGAG AGGGAGGGTA GAGGA 25

<210> 79

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Unsure

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ACGTGGCTTC TGTGCTTGCT GC 22

<210> 80

<211> 25

<212> DNA

<213> Unknown

<220>

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<210> 81

<211> 26

<212> DNA

<213> Unknown

<220>

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TTGCCCTTCT CCTGCCCAAG CGGCCC 26

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GGCGGGGGCT GCAAGTCGTA CCCATCG 27

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CGGCACTCCA TGGAGATCCG CACCCCT 27

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CAGGCAGGAT TGATGTCAGG GGTGCGG 27



<210> 85

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CATGGAGTGC CGATGGGTAC GACTTGC 27

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GGCCTCCTCG GAGGAGCCAA GGGATGA 27

<210> 87

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<220>

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GGGAAAGGAG CCCGAAGGAG AGGAGAG 27

<210> 88

<211> 25

<212> DNA

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<220>

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CCTGCTGGCC ATTCTCCTGT CTTAC 25

<210> 89

<211> 25

<212> DNA

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GGGTCCAGGT CCCGCAGAAG GTTGA 25

<210> 90

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GAAGACGGAG CATGGCCCTG AAGAC 25

<210> 91

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<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 91

GGCAGCTCAG TTGGCCAAGT CCAGT 25

<210> 92

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 92

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Cys  
1 5 10 15

<210> 93

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<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 93

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
1 5 10 15

<210> 94

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 94

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly  
1 5 10 15

<210> 95

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 95

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<210> 96  
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<212> DNA  
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<220>  
<223> Unsure  
<400> 96

GCTGACTCGA CAGCACTGTC TTCTCGAGCT G 31

<210> 97  
<211> 21  
<212> DNA  
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<220>  
<223> Unsure  
<400> 97

AACCCCTTCA TCTATGCGTG G 21

<210> 98  
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<212> DNA  
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<223> Unsure  
<400> 98

ATATTCTGGC CATGAGGCAC 20

<210> 99  
<211> 28  
<212> DNA  
<213> Unknown  
<220>  
<223> Unsure

<400> 99

TTCCGAGAGG AGCTACGCAA GATGCTTC 28

Ans  
B1  
af

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